

Structure of LCP1 and alignments of domains

FIG. 1A



FIG. 1B

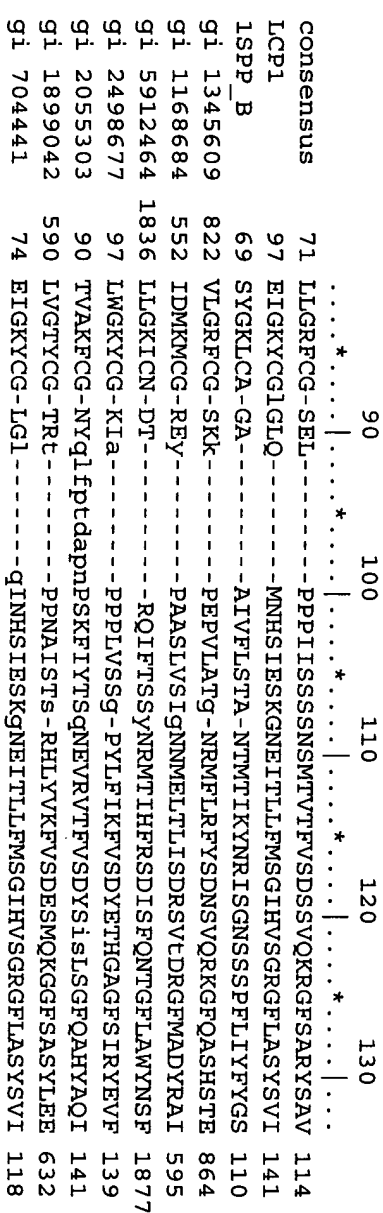
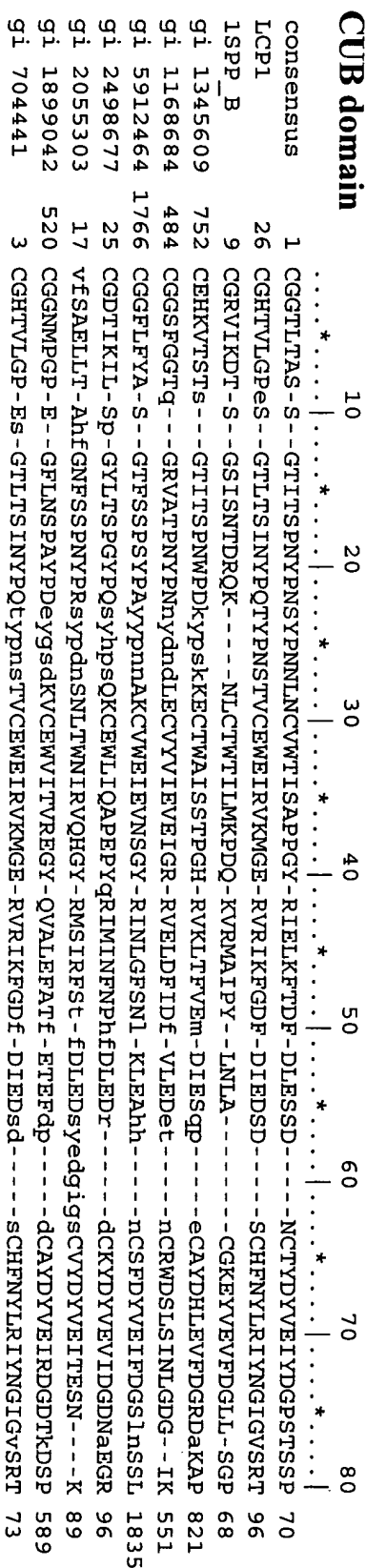


FIG. 1C

LCCL domain

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consensus      1 QAVTCDTKALDLC---KPVTDGNRVHCPAGCLLPK---AKVFGTL---VYASLSSICRAVHAGVIDNTSGGAVDVVRVGG 72
LCPI           145 dLITCLDTASNFL---EPEFSK---YCPAGCLLPF---AEISGTLphGYRDSPLCMAGVHAGVVSNTLGGQISVVISKG 215
gi 12053227    387 QDLDCYTTVAQLCPfEKPATHCPRIHCPAHCKDEPSYwAPVFGTN---IYADTSSICKTAVHAGVISNESGGDYDVPYDK 464
gi 12002311    291 QIVSCEVRLRDQC---KGTT-CNRYECPAGCLDSK---AKVIGSV---HYEMQSSICRAAIHYGIIDND--GGVVDITRQGR 360
gi 12002311    392 QAVTCETTVEQLCPfhKPASHCPRVYCPRNCMQANphYARVIGTR--VYSDLSSICRAVHAGVVRNH--GGYVDVPYDK 468
gi 12053227    286 QVVRCDTKMKDRC---KGST-CNRYQCPAGCLNHK---AKIFGTL---FYESSSSICRAAIHYGIIDDK--GGLVDITRNGK 355
gi 7387581     26 NAITCFTTRGLDLR---KETED---VLCRANCPLMQ---FYVFGDG---IYASLSSVCGAAIHRGVITN--AGGAVRVQTLPG 93
gi 12644458    32 IPVTCFTTRGLDIR---KEKAD---VLCRPGGCSLEE---FSVFGNI---VYASVSSICGAHVHRGVIGT--SGGPVRVYSLPG 99
gi 7044441     126 LFGHCIOQFFWNLS---SVST---APAGCLLPF---AEISGTLphGYRDSPLCMAGVHAGVVSNTLGGQISVVISKG 193
gi 913964      391 REVDCDSKAVDFL---DDVGEPRRIHCPAGCSLTA---GTWVGTA---IYHELSSVCRAAIHAGKLPN--SGGAVHVVANNGP 461
gi 6624095     42 PQINCDVKAGKII---DPEFI---VKCPAGCQDPK---YHVGTD---VYASYSVCGAAVHSGVLDN--SGGKILVRKVAG 109

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90

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consensus      73 QPYIIGSLANGIQSE 87
LCPI           216 IPYESSLANNVTSV 230
gi 12053227    465 KKTIVGSLRNGVQSE 479
gi 12002311    361 KHYFIKSNRNGIQTI 375
gi 12002311    469 RKTIVASFQNGIFSE 483
gi 12053227    356 VPFFVKSERHGVQSL 370
gi 7387581     94 QENYPAVHANGIQSQ 108
gi 12644458    100 RENYSSVDANGIQSQ 114
gi 7044441     194 IPYESSLANNVTSV 208
gi 913964      462 YSDFLGSDLNGIKSE 476
gi 6624095     110 QSGYKGSYSNGVQSL 124

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FIG. 1D **DSD/FA58C domain**

consensus	1	PLGMESG-RIPDSQITASSS-----YSAN-----WTPENARLNSQGAGAMSPK---ANDQNQWLQVDLGGKPRRYT	62
LCPI	249	tlGMESG-VIADPQITASSVlewthtgQENS-----WKPKARLKKPPD--WAAF---ATDEYQWLQIDLNKEKKIT	316
LCZI_A	5	PLGMENG-KIENKQITASSF-----KKSwwg--dYMEPRARLNAQGRVNAWQAK---ANNNKQWLIEDLKIKIKIT	70
LD7P_M	7	PLGMESK-AISDAQITASSY-----FTNWfa---twSPSKARLHLQGRSNARWPQ---VNNPKEWLQVDFQKTMKYT	71
gi 2547128	280	PLGMESG-RIANEQISASST-----FSDgr-----WTPQQRHLGGD--NGWTPN---LDSNKEYLQVDLRFITMLT	340
gi 2506380	233	PLGLKNN-SIPDKQITASSS-----YKTWghlfswnpsYARLDKQGNFNNAVAG---SYGNDQWLQVDLGGSSKEYT	300
gi 127058	311	PLGLKNN-TIPDSQMSASSS-----YKThnlrafgwyPHLGRLDNQKINAWTAQ---SNSAKEWLQVDLGTQRQVT	378
gi 2645493	2035	PLGMASG-HIRDFQITASGQ-----YGQ-----WAPKLARLHYSGSINAWSTKd--PFS---WIKVDLLAPMI IH	2093
gi 2623894	322	PLGMKSG-HIQDYQITASSV-----FRtlmdmftwEPKARLDKQGNVNAWTSg---HNDQSQWLQVDLVPPTKYT	389
gi 704441	228	TLGMESGgDRGSSNNSITVL-----EWTdhtgqenswKP--KKSQAEK--TWTAldgaFATDEYQWLQIDLNKEKKIT	295

consensus	63	GVITQGRKDFGSS--QWVTSYKQYSDDERTWTTYKGDG-GKPKIFPGNSDRNT-PVTNDFDPPiVARYIRILPLTWHG	137
LCPI	317	GIITGSTMEHN--YVVSAYRILYSDDGQKWTVYREPGEQDKIFQGNKDYHQ-DYRNNFLPILARFIRVNPQWQ	392
LCZI_A	71	AIITQGCKSLSE--MYVKSytiHYSEQGVEMKPYRLKSMDVKIFEGNTNITKG-HYKNFENPILISRfIRVlPKTMNQ	146
LD7P_M	72	GVTTQGVKSLITS--MYVKEFLISSQDGHQWTLFFQN--GKVKVFQGNQDSFT--PVVNCILDPPILTRYLRIHPQSWH	145
gi 2547128	341	AIATQGAISRETQK-gYVVKSYKLEVSTNGEDWVYRHG--KNHKIFQANNDATe-VVlNKlHMPILTRfIRIRPQTWHL	416
gi 2506380	301	GIITQGARNFSGV--QFVASYKVAYSNDSANWTEYQDPRtgSSKIFPGNWDNHS-HKKNLfETPILARyRILPVAMHN	376
gi 127058	379	GIITQGARDFGHI--QYVESYKVAHSDDGQWTVYEEQ--GSSKVFQGNULDNNs-HKKNIfeKPFMARyRVLpVSWHN	452
gi 2645493	2094	GIIMTQGARQKFSS--LYVSQFIIMYSLDGNKWSYRGNSGTILMVFFGNVDSSG-IKHNIENPILIAQYIRLHPThYSI	2169
gi 2623894	390	GIITQGAKDfGHV--QFVGSYKLAYSNDGEHWMVHQDEKqRKDKVFQGNFNDNT-HRKNVlDPPiYARfIRILPWSWYG	465
gi 704441	296	GIITGSTMVSTltmclPTESCTVMGRNGL-CTESlVVe-QD-KIFQGNKRIITfMVVRNNFLPILAR-----	361

consensus	138	RI	139
LCPI	393	KI	394
LCZI_A	147	SI	148
LD7P_M	146	QI	147
gi 2547128	417	GI	418
gi 2506380	377	RI	378
gi 127058	453	RI	454
gi 2645493	2170	RS	2171
gi 2623894	466	RI	467
gi 704441	362	-L	362

Structure of the LCP gene (Chr. 3q12.1)

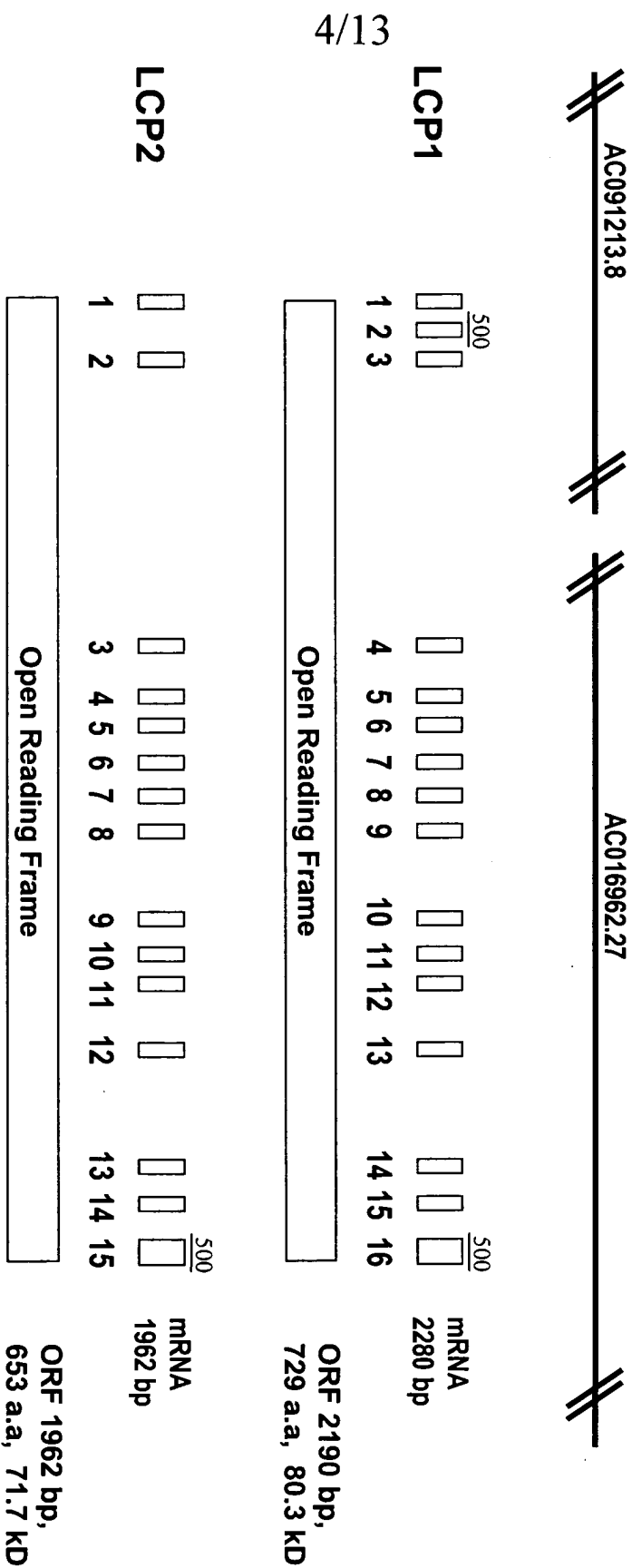


FIG. 2

ut: SEQ ID NO: 1

aa: SEQ ID NO: 3

FIG. 3

[illegible]

FIG. 3

176	Y	C	P	A	G	C	L	L	P	F	A	E	I
603	TAC	TGC	CCA	GCT	GCT	TGT	CTG	CTT	CCT	TTT	GCT	GAG	ATA
189	S	G	T	I	P	H	G	Y	R	D	S	S	P
642	TCT	GGA	ACA	ATT	CCT	CAT	GGA	TAT	AGA	GAT	TCC	TCG	CCA
202	L	C	M	A	G	V	H	A	G	V	V	S	N
681	TTG	TGC	ATG	GCT	GCT	GTT	GCA	GTA	GTA	GTG	TCA	AAC	
215	T	L	G	G	G	Q	I	S	V	V	I	S	K
720	ACG	TTG	GGC	GGC	CAA	ATC	AGT	GTT	GTA	ATT	AGT	AAA	GGT
228	I	P	Y	Y	E	S	S	L	A	N	N	V	T
759	ATT	CCC	TAT	TAT	GAA	AGT	TCT	TTG	GCT	AAC	AAC	GTG	ACA
241	S	V	V	G	H	L	S	T	S	L	F	T	F
798	TCT	GTG	GTG	GGA	CAC	TTA	TCT	ACA	AGT	CTT	TTT	ACA	TTT
254	K	T	S	G	C	Y	G	T	L	G	M	E	S
837	AAG	ACA	AGT	GGA	TGT	TAT	GGA	ACA	CTG	GGG	ATG	GAG	TCT
267	G	V	I	A	D	P	Q	I	T	A	S	S	V
876	GGT	GTG	ATC	GCG	GAT	CCT	CAA	ATA	ACA	GCA	TCA	TCT	GTG
280	L	E	W	T	D	H	T	G	Q	E	N	S	M
915	CTG	GAG	TGG	ACT	GAC	CAC	ACA	GGG	CAA	GAG	AAC	AGT	TGG
293	K	P	K	K	A	R	L	K	K	P	G	P	P
954	AAA	CCC	AAA	AAA	GCC	AGG	CTG	AAA	AAA	CCT	GGA	CCG	CCT
306	W	A	A	F	A	T	D	E	Y	Q	W	L	Q
993	TGG	GCT	GCT	TTT	GCC	ACT	GAT	GAA	TAC	CAG	TGG	TTA	CAA
319	I	D	L	N	K	K	E	K	K	I	T	G	I
1032	ATA	GAT	TTG	AAT	AAG	GAA	AAG	AAA	ATA	ACA	GGC	ATT	ATA
332	T	T	G	S	T	M	V	E	H	N	Y	Y	V
1071	ACC	ACT	GGA	TCC	ACC	ATG	GTG	GAG	CAC	AAT	TAC	TAT	GTG
345	S	A	Y	R	I	L	Y	S	D	D	G	Q	K
1110	TCT	GCC	TAC	AGA	ATC	CTG	TAC	AGT	GAT	GAT	GGG	CAG	AAA
358	W	T	V	Y	R	E	P	G	V	E	Q	D	K
1149	TGG	ACT	GTG	TAC	AGA	GAG	CCT	GGT	GTG	GAG	CAA	GAT	AAG
371	I	F	Q	G	N	K	D	Y	H	Q	D	V	R
1188	ATA	TTT	CAA	GGA	AAC	AAA	GAT	TAT	CAC	CAG	GAT	GTG	CGT
384	N	N	F	L	P	P	I	I	A	R	F	I	R
1227	AAT	AAC	TTT	TTG	CCA	CCA	ATT	ATT	GCA	CGT	TTT	ATT	AGA

FIG. 3

1266	V	N	P	T	Q	W	Q	Q	K	I	A	M	K	397
410	M	E	L	L	G	C	Q	F	I	P	K	G	R	410
1305	ATG	GAG	CTG	CTC	GGA	TGT	CAG	TTT	ATT	CCT	AAA	GGT	CGT	1305
423	P	P	K	L	T	Q	P	P	P	P	R	N	S	423
1344	CCT	CCA	AAA	CCT	ACT	CAA	CCT	CCA	CCT	CGG	AAC	AGC		1344
436	N	D	L	K	N	T	T	A	P	P	K	I	A	436
1383	AAT	GAC	CTC	AAA	AAC	ACT	ACA	GCC	CCT	CCA	AAA	ATA	GCC	1383
449	K	G	R	A	P	K	F	T	Q	P	L	Q	P	449
1422	AAA	GGT	CGT	GCC	CCA	AAA	TTT	ACG	CAA	CCA	CTA	CAA	CCT	1422
462	R	S	S	N	E	F	P	A	Q	T	E	Q	T	462
1461	CGC	AGT	AGC	AAT	GAA	TTT	CCT	GCA	CAG	ACA	GAA	CAA	ACA	1461
475	T	A	S	P	D	I	R	N	T	T	V	T	P	475
1500	ACT	GCC	AGT	CCT	GAT	ATC	AGA	AAT	ACT	ACC	GTA	ACT	CCA	1500
488	N	V	T	K	D	V	A	L	A	A	V	L	V	488
1539	AAT	GTA	ACC	AAA	GAT	GTA	GCG	CTG	GCT	GCA	GTT	CTT	GTC	1539
501	P	V	L	V	M	V	L	T	T	L	I	L	I	501
1578	CCT	GTG	CTG	CTG	ATG	GTC	CTC	ACT	ACT	CTC	ATT	CTC	ATA	1578
514	L	V	C	A	W	H	W	R	N	R	K	K	K	514
1617	TTA	GTG	TGT	GCT	TGG	CAC	TGG	AGA	AAC	AGA	AAG	AAA	AAA	1617
527	T	E	G	T	Y	D	L	P	Y	W	D	R	A	527
1656	ACT	GAA	GGC	ACC	TAT	GAC	TTA	CCT	TAC	TGG	GAC	CGG	GCA	1656
540	G	W	W	K	G	M	K	Q	F	L	P	A	K	540
1695	GGT	TGG	TGG	AAA	GGA	ATG	AAG	CAG	TTT	CTT	CCT	GCA	AAA	1695
553	A	V	D	H	E	E	T	P	V	R	Y	S	S	553
1734	GCA	GTG	GAC	CAT	GAG	GAA	ACC	CCA	GTT	CGC	TAT	AGC	AGC	1734
566	S	E	V	N	H	L	S	P	R	E	V	T	T	566
1773	AGC	GAA	GTT	AAT	CAC	CTG	AGT	CCA	AGA	GAA	GTC	ACC	ACA	1773
579	V	L	Q	A	D	S	A	E	Y	A	Q	P	L	579
1812	GTG	CTG	CTG	CAG	GCT	GAC	TCT	GCA	GAG	TAT	GCT	CAG	CTG	1812
592	V	G	G	I	V	G	T	L	H	Q	R	S	T	592
1851	GTA	GGA	GGA	GGA	ATT	GTT	GGT	ACA	CTT	CAT	CAA	AGA	TCT	1851
605	F	K	P	E	E	G	K	E	A	G	Y	A	D	605
1890	TTT	AAA	CCA	GAA	GAA	GAA	AAA	GAA	GCA	GGC	TAT	GCA	GAC	1890
618	L	D	P	Y	N	S	P	G	Q	E	V	Y	H	618
1929	CTA	GAT	CCT	TAC	AAC	TCA	CCA	GGG	CAG	GAA	GTT	TAT	CAT	1929

FIG. 3

631	A	Y	A	E	P	L	P	I	T	G	P	E	Y
1968	GCC	TAT	GCT	GAA	CCA	CTC	CCA	ATT	ACG	GGG	CCT	GAG	TAT
644	A	T	P	I	I	M	D	M	S	G	H	P	T
2007	GCA	ACC	CCA	ATC	ATC	ATG	GAC	ATG	TCA	GGG	CAC	CCC	ACA
657	T	S	V	G	Q	P	S	T	S	T	F	K	A
2046	ACT	TCA	GTT	GGT	CAG	CCC	TCC	ACA	TCC	ACT	TTC	AAG	GCT
670	T	G	N	Q	P	P	P	L	V	G	T	Y	N
2085	ACG	GGG	AAC	CAA	CCT	CCC	CCA	CTA	GTG	GGA	ACT	TAC	AAT
683	T	L	L	S	R	T	D	S	C	S	S	A	Q
2124	ACA	CTT	CTC	TCC	AGG	ACT	GAC	AGC	TGC	TCC	TCA	GCC	CAG
696	A	Q	Y	D	T	P	K	A	G	K	P	G	L
2163	GCC	CAG	TAT	GAT	ACC	CCG	AAA	GCT	GGG	AAG	CCA	GGT	CTA
709	P	A	P	D	E	L	V	Y	Q	V	P	Q	S
2202	CCT	GCC	CCA	GAC	GAA	TTG	GTG	TAC	CAG	GTG	CCA	CAG	AGC
722	T	Q	E	V	S	G	A	G	R	D	G	E	C
2241	ACA	CAA	GAA	GTA	TCA	GGA	GCA	GGA	AGG	GAT	GGG	GAA	TGT
730	D	V	F	K	E	I	L	*					
2280	GAT	GTT	TTT	AAA	GAA	ATC	CTT	TGA	agatg	atg	ctg	ctt	ctt

LCP2

nt: SEQ ID NO: 1113
 aa: SEQ ID NO: 1114

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M P L F L L L L L L V L L L
ATG CCT CTG TTC CTC CTC CTC TTA CTT GTC CTC CTC CTG
CTG CTC GAG GAC GCT GGA GCC CAG CAA GGC AAA TAC TGT
G L G L Q M N H S I E S K
GGT CTG GGG TTG CAA ATG AAC CAT TCA ATT GAA TCA AAA
G N E I T L L F M S G I H
GGC AAT GAA ATC ACA TTG CTC TTC ATG AGT GGA ATC CAT
V S G R G F L A S S Y S V I
GTT TCT GGA CGC GGA TTT TTG GCC TCA TAC TCT GTT ATA
D K Q D L I T C L D T A S
GAT AAA CAA GAT CTA ATT ACT TGT TTG GAC ACT GCA TCC
N F L E P E F S K Y C P A
AAT TTT TTG GAA CCT GAG TTC AGT AAG TAC TGC CCA GCT
G C L L P F A E I S G T I
GGT TGT CTG CTT CCT TTT GCT GAG ATA TCT GGA ACA ATT
P H G Y R D S S P L C M A
CCT CAT GGA TAT AGA GAT TCC TCG CCA TTG TGC ATG GCT
G V H A G V V S N T L G G
GGT GTG CAT GCA GGA GTA GTG TCA AAC ACG TTG GGC GGC
Q I S V V I S K G I P Y Y
CAA ATC AGT GTT GTA ATT AGT AAA GGT ATT CCC TAT TAT
E S S L A N N V T S V V G
GAA AGT TCT TTG GCT AAC AAC GTC ACA TCT GTG GGA

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FIG. 4

FIG. 4

169	H	L	S	T	S	L	F	T	F	T	A	ACA	TTT	ACA	TTT	AAG	ACA	AGT	GGA
507	CAC	TTA	TCT	ACA	AGT	CTT	TTT	ACA	TTT	AAG	ACA	AGT	GGA						
182	C	Y	G	T	L	G	M	E	S	G	V	I	A						
546	TGT	TAT	GGA	ACA	CTG	GGG	ATG	GAG	TCT	GGT	GTG	ATC	GCG						
195	D	P	Q	I	T	A	S	S	V	L	E	W	T						
585	GAT	CCT	CAA	ATA	ACA	GCA	TCA	TCT	GTG	CTG	GAG	TGG	ACT						
208	D	H	T	G	Q	E	N	S	W	K	P	K	K						
624	GAC	CAC	ACA	GGG	CAA	GAG	AAC	AGT	TGG	AAA	CCC	AAA	AAA						
221	A	R	L	K	K	P	G	P	P	W	A	A	F						
663	GCC	AGG	CTG	AAA	AAA	CCT	GGA	CCG	CCT	TGG	GCT	GCT	TTT						
234	A	T	D	E	Y	Q	W	L	Q	I	D	L	N						
702	GCC	ACT	GAT	GAA	TAC	CAG	TGG	TTA	CAA	ATA	GAT	TTG	AAT						
247	K	E	K	K	I	T	G	I	I	T	T	G	S						
741	AAG	GAA	AAG	AAA	ATA	ACA	GGC	ATT	ATA	AAC	ACT	GGA	TCC						
260	T	M	V	E	H	N	Y	Y	V	S	A	Y	R						
780	ACC	ATG	GTG	GAG	CAC	AAT	TAC	TAT	GTG	TCT	GCC	TAC	AGA						
273	I	L	Y	S	D	D	G	Q	K	W	T	V	Y						
819	ATC	CTG	TAC	AGT	GAT	GAT	GGG	CAG	AAA	TGG	ACT	GTG	TAC						
286	R	E	P	G	V	E	Q	D	K	I	F	Q	G						
858	AGA	GAG	CCT	GGT	GTG	GAG	CAA	GAT	AAG	ATA	TTT	CAA	GGA						
299	N	K	D	Y	H	Q	D	V	R	N	N	F	L						
897	AAC	AAA	GAT	TAT	CAC	CAG	GAT	GTG	CGT	AAT	AAC	TTT	TTG						
312	P	P	I	I	A	R	F	I	R	V	N	P	T						
936	CCA	CCA	ATT	ATT	GCA	CGT	TTT	ATT	AGA	GTG	AAT	CCT	ACC						
325	Q	W	Q	Q	K	I	A	M	K	M	E	L	L						
975	CAA	TGG	CAG	CAA	AAA	ATT	GCC	ATG	AAA	ATG	GAG	CTG	CTC						
338	G	C	Q	F	I	P	K	G	R	P	P	K	L						
1014	GGA	TGT	CAG	TTT	ATT	CCT	AAA	GGT	CGT	CCT	CCA	AAA	CTT						

FIG. 4

351	T	Q	P	P	P	P	R	N	S	N	D	L	K	1053
364	N	T	T	A	P	P	K	I	A	K	G	R	A	1092
377	P	K	F	T	Q	P	L	Q	P	R	S	S	N	1131
390	E	F	P	A	Q	T	E	Q	T	A	S	P		1170
403	D	I	R	N	T	T	V	T	P	N	V	T	K	1209
416	D	V	A	L	A	A	V	L	V	P	V	L	V	1248
429	M	V	L	T	T	L	I	L	I	L	V	C	A	1287
442	W	H	W	R	N	R	K	K	K	T	E	G	T	1326
455	Y	D	L	P	Y	W	D	R	A	G	W	W	K	1365
468	G	M	K	Q	F	L	P	A	K	A	V	D	H	1404
481	E	E	T	P	V	R	Y	S	S	S	E	V	N	1443
494	H	L	S	P	R	E	V	T	T	V	L	Q	A	1482
507	D	S	A	E	Y	A	Q	P	L	V	G	G	I	1521
520	V	G	T	L	H	Q	R	S	T	F	K	P	E	1560
533	E	G	K	E	A	G	Y	A	D	L	D	P	Y	

FIG. 4

1599	GAA	GGA	AAA	GAA	GCA	GGC	TAT	GCA	GAC	CTA	GAT	CCT	TAC
546	N	S	P	G	Q	E	V	Y	H	A	Y	A	E
1638	AAC	TCA	CCA	GGG	CAG	GAA	GTT	TAT	CAT	GCC	TAT	GCT	GAA
559	P	L	P	I	T	G	P	E	Y	A	T	P	I
1677	CCA	CTC	CCA	ATT	ACG	GGG	CCT	GAG	TAT	GCA	ACC	CCA	ATC
572	I	M	D	M	S	G	H	P	T	T	S	V	G
1716	ATC	ATG	GAC	ATG	TCA	GGG	CAC	CCC	ACA	ACT	TCA	GTT	GGT
585	Q	P	S	T	S	T	F	K	A	T	G	N	Q
1755	CAG	CCC	TCC	ACA	TCC	ACT	TTC	AAG	GCT	ACG	GGG	AAC	CAA
598	P	P	P	L	V	G	T	Y	N	T	L	L	S
1794	CCT	CCC	CCA	CTA	GTG	GGA	ACT	TAC	AAT	ACA	CTT	CTC	TCC
611	R	T	D	S	C	S	S	A	Q	A	Q	Y	D
1833	AGG	ACT	GAC	AGC	TGC	TCC	TCA	GCC	CAG	GCC	CAG	TAT	GAT
624	T	P	K	A	G	K	P	G	L	P	A	P	D
1872	ACC	CCG	AAA	GCT	GGG	AAG	CCA	GGT	CTA	CCT	GCC	CCA	GAC
637	E	L	V	Y	Q	V	P	Q	S	T	Q	E	V
1911	GAA	TTG	GTG	TAC	CAG	GTG	CCA	CAG	AGC	ACA	CAA	GAA	GTA
650	S	G	A	G	R	D	G	E	C	D	V	F	K
1950	TCA	GGA	GCA	GGA	AGG	GAT	GGG	GAA	TGT	GAT	GTT	TTT	AAA
654	E	I	L	*									
1962	GAA	ATC	CTT	TGA									

Tissue Expression profile of LCP

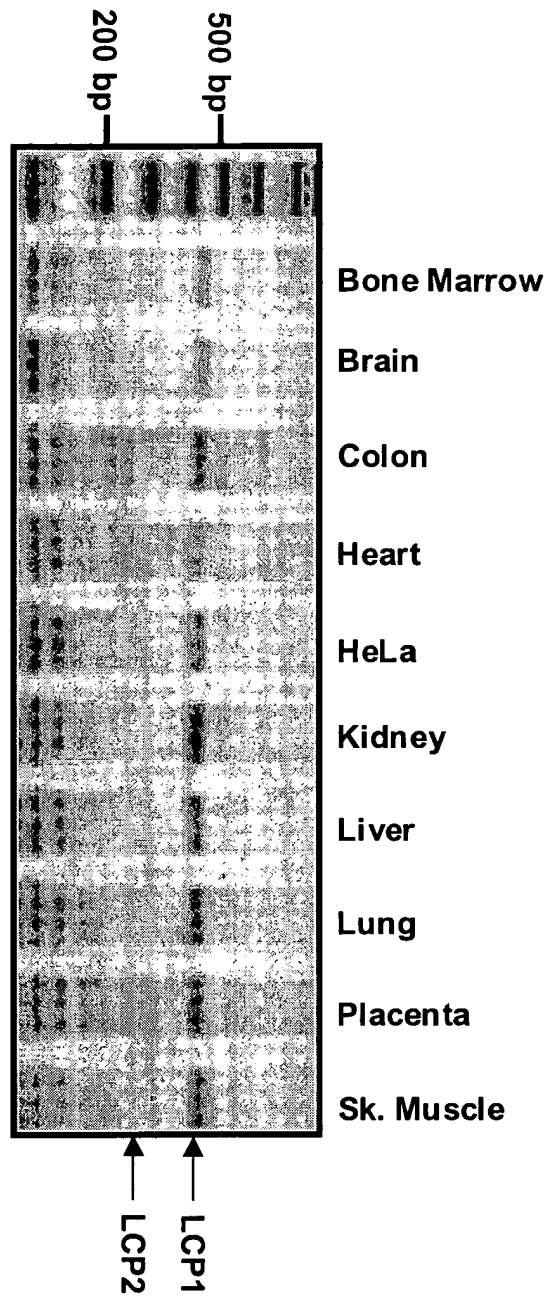


FIG. 5